

SEQUENCE LISTING

<110> KIRIN BEER KABUSHIKI KAISHA

National Institute of Advanced Industrial Science and Technology

<120> A methylotrophic yeast capable of producing a mammalian type sugar chain

<130> PH-1796-PCT

<150> JP 2002-127677

<151> 2002-04-26

<160> 120

<170> PatentIn Ver. 2.0

<210> 1

<211> 11

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 1

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<210> 2

<211> 11

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

Asp Gly Pro Ser His Lys Asp Trp Arg Gly Gly

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<210> 3

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PGP5 for amplification of
5'-region of Ogataea minuta GAP gene

<400> 3

gcntayatgt tyaartayga ywsnacncay gg

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<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PGP3 for amplification of
3'-region of Ogataea minuta GAP gene

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<210> 5

<211> 3186

<212> DNA

<213> *Ogataea minuta*

<220>

<221> CDS

<222> 1492..2502

<400> 5

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<210> 6

<211> 336

<212> PRT

<213> *Ogataea minuta*

<400> 6

Met Ala Tyr Asn Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu

1

5

10

15

Val Leu Arg Ile Ala Leu Ser Arg Lys Asp Ile Asn Val Val Ala Val

20

25

30

Asn Asp Pro Phe Ile Ala Ala Glu Tyr Ala Ala Tyr Met Phe Lys Tyr

35

40

45

Asp Ser Thr His Gly Arg Tyr Gln Gly Glu Val Thr Phe Glu Gly Lys

50

55

60

Tyr Leu Val Ile Asp Gly Gln Lys Ile Glu Val Phe Gln Glu Arg Asp

65

70

75

80

Pro Ala Asp Ile Pro Trp Gly Lys Glu Gly Val Asp Phe Val Ile Asp

85

90

95

Ser Thr Gly Val Phe Thr Thr Thr Ala Gly Ala Gln Lys His Ile Asp

100

105

110

Ala Gly Ala Lys Lys Val Ile Ile Thr Ala Pro Ser Ala Asp Ala Pro

115

120

125

Met Phe Val Met Gly Val Asn His Lys Glu Tyr Thr Lys Asp Leu Ser

130

135

140

Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala

145

150

155

160

Lys Val Val Asn Asp Val Phe Gly Ile Glu Ser Gly Leu Met Thr Thr

165

170

175

Val His Ser Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His

180

185

190

Lys Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser

195

200

205

Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Ala Leu Ala

210

215

220

Gly Lys Leu Thr Gly Met Ser Leu Arg Val Pro Thr Thr Asp Val Ser

225

230

235

240

Val Val Asp Leu Thr Val Asn Leu Lys Thr Pro Thr Thr Tyr Ala Glu

245

250

255

Ile Ser Ala Ala Ile Lys Lys Ala Ser Glu Gly Glu Leu Ala Gly Ile

260

265

270

Leu Gly Tyr Thr Glu Asp Ala Val Val Ser Thr Asp Phe Leu Thr Asp

275

280

285

Asn Arg Ser Ser Ile Phe Asp Ala Ser Ala Gly Ile Leu Leu Thr Pro

290

295

300

Thr Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser

305

310

315

320

Thr Arg Val Val Asp Leu Leu Glu His Val Ala Lys Val Ser Ser Ala

325

330

335

<210> 7

<211> 1491

<212> DNA

<213> *Ogataea minuta*

<400> 7

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<210> 8

<211> 524

<212> DNA

<213> *Ogataea minuta*

<400> 8

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atgtgctctt ctgctTTTTT ggtgaccaa cgagatgaca attgactgca ttgaaaaggt 480
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<210> 9

<211> 113

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for production of an expression cassette with GAP gene promoter and terminator from Ogataea minuta

<400> 9

gtttgaattc actcaattaa catacacaaa tacaatacaa agtcgacaaa aaatgcatgt 60
ggatagatga ccaatggcct ctttaagtaa acatttcggt ttgaatatat ttc 113

<210> 10

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for production of an

expression cassette with GAP gene promoter and terminator from Ogataea minuta

<400> 10

tttttactag tacggtaccg ctcgaaatcga cacaggag

38

<210> 11

<211> 12

<212> PRT

<213> Saccharomyces cerevisiae

<400> 11

Gly Pro Tyr Ile Cys Leu Val Lys Thr His Ile Asp

1

5

10

<210> 12

<211> 11

<212> PRT

<213> Saccharomyces cerevisiae

<400> 12

Gly Arg Gly Leu Phe Gly Lys Gly Arg Asp Pro

1

5

10

<210> 13

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PUR5 for amplification of 5'-region of Ogataea Minuta URA3 gene

<400> 13

ggncntaya thtgyytngt naaracncay athga

35

<210> 14

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PUR3 for amplification of 3'-region of Ogataea Minuta URA3 gene

<400> 14

ggrtcncnc cyttncraa narncnckn cc

32

<210> 15

<211> 3113

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1732..2529

<400> 15

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<210> 16

<211> 265

<212> PRT

<213> *Ogataea minuta*

<400> 16

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20 25 30

Leu Cys Ala Ser Val Asp Leu Thr Ser Thr Lys Asp Leu Leu Glu Leu

35 40 45

Leu Asp Lys Leu Gly Pro Phe Ile Cys Leu Val Lys Thr His Ile Asp

50 55 60

Ile Val Glu Asp Phe Ser Tyr Glu Asn Thr Val Val Pro Leu Leu Lys

65 70 75 80

Leu Ala Lys Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala

85 90 95

Asp Ile Gly Asn Thr Val Lys Leu Gln Tyr Lys Gly Gly Val Tyr Gln

100 105 110

Ile Ala Lys Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Ser

115 120 125

Arg Ile Val Ser Gly Leu Arg Gln Ala Ala Gln Glu Thr Thr Asp Glu

130 135 140

Pro Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Glu Gly Ser Leu

145 150 155 160

Ala Tyr Gly Glu Tyr Thr Lys Lys Thr Val Glu Ile Ala Lys Ser Asp

165

170

175

Arg Asp Phe Val Ile Gly Phe Ile Ala Gln Asn Asp Met Gly Gly Arg

180

185

190

Asp Glu Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp

195

200

205

Asp Thr Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Ser Ala Val

210

215

220

Met Lys Thr Gly Thr Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Gly

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Lys Gly Arg Asp Pro Val Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly

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250

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Trp Asp Ala Tyr Leu Ser Arg Val Ala

260

265

<210> 17

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of a gene

fragment conferring resistance against chloramphenicol

<400> 17

atggagaaaa aaactagtgg atataccacc

30

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of a gene fragment conferring resistance against chloramphenicol

<400> 18

ctgagacgaa aaagatatct caataaaccc

30

<210> 19

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DU5 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 19

aggaagaaga ggaggaagag gaagaaac

28

<210> 20

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DUC5 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 20

cgatgccatt gggatatatc aacgggtgg

28

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DU3 used for confirmation of destruction of Ogataea minuta URA3 gene

<400> 21

ccgtgtttga gtttgtgaaa aaccagggc

29

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DUC3 used for confirmation
of destruction of Ogataea minuta URA3 gene

<400> 22

tgtggcgtgt tacggtgaaa acctggcc

28

<210> 23

<211> 14

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 23

Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met

1

5

10

<210> 24

<211> 14

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

Gln Asp Ser Tyr Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr

1

5

10

<210> 25

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAD5 for amplification of 5'-region of Ogataea minuta ADE1 gene

<400> 25

ttygtngcna cngaymgntat hwsngcntay gaygtnatha tg 42

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAD3 for amplification of 3'-region of Ogataea minuta ADE1 gene

<400> 26

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<210> 27

<211> 2560

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 939..1850

<400> 27

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tgcgtgtggg cacgaacgag cccacgtaga caaacaggct caaagccaac gaaaactcgt 180
acgcagtcac catcaattcc agaaagtctt cgtggatgaa cgacagctca ggaaggttga 240
actttgtgag ataagctctg ctggcaagaa ttcccacgag aagagtgtc aattctttcc 300
cgttgacgag atagttgagc ttgtttccgt ctgtaacag gactccctct ttatggtagc 360
caggcatcac aagatccacc aacgtcagag tgaagaacca caccaggtaa accttcagc 420
acgtgacatt taacacaaga tcccgccagt tgccgactat cttggactcg aaaagcgttt 480
tcagcgtggc aaaatcgatg cttgcgcctt caaccacata ctctcatta cagcaaaagt 540
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agaaatcttt atgcgtagtc ttgggggttca attcagacat ggtagattgg tgagggtaat 660
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<210> 28

<211> 303

<212> PRT

<213> Ogataea minuta

<400> 28

Met Ser Leu Thr Thr Thr Asn Leu Asp Gly Ile Leu Pro Leu Ile Ala

1

5

10

15

Lys Gly Lys Val Arg Asp Ile Tyr Gln Val Asp Glu Glu Ser Leu Leu

20

25

30

Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met Glu Asn

35

40

45

Gly Ile Lys Asp Lys Gly Lys Ile Leu Thr Gln Leu Ser Val Phe Trp

50

55

60

Phe Asp Leu Leu Lys Asp Thr Ile Lys Asn His Leu Ile Ala Ser Thr

65

70

75

80

Asp Asp Glu Val Phe Ala Arg Leu Pro Gln Glu Leu Ser Gln Pro Lys

85

90

95

Tyr Lys Ser Gln Leu Ser Gly Arg Ala Leu Val Val Arg Lys His Lys

100

105

110

Leu Ile Pro Leu Glu Val Ile Val Arg Gly Tyr Ile Thr Gly Ser Ala

115

120

125

Trp Lys Glu Tyr Asn Lys Ser Lys Thr Val His Gly Leu Glu Val Gly

130

135

140

Ala Glu Leu Lys Glu Ser Gln Glu Phe Pro Val Pro Ile Phe Thr Pro

145

150

155

160

Ser Thr Lys Ala Glu Gln Gly Glu His Asp Glu Asn Ile Ser Pro Glu

165

170

175

Lys Ala Ala Glu Ile Val Gly Glu Gln Leu Cys Ala Arg Leu Ala Glu

180

185

190

Lys Ala Val Gln Leu Tyr Ser Lys Ala Arg Thr Tyr Ala Lys Ser Lys
195 200 205

Gly Ile Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asn
210 215 220

Asp Glu Leu Val Leu Val Asp Glu Val Leu Thr Pro Asp Ser Ser Arg
225 230 235 240

Phe Trp Asp Ala Lys Thr Tyr Lys Ile Gly Gln Ser Gln Asp Ser Tyr
245 250 255

Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr Ser Asn Gly Leu Asn Gly
260 265 270

Lys Asp Gly Val Ser Met Thr Ala Glu Ile Ala Glu Arg Thr Gly Ala
275 280 285

Lys Tyr Val Glu Ala Phe Glu Ser Leu Thr Gly Arg Lys Trp Thr
290 295 300

<210> 29

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5'-primer for amplification of

upstream region of URA3 structural gene

<400> 29

ccccgagctc aaaaaaaagg taccaatttc agctccgacg ccggagccca ctacgcctac 60

<210> 30

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 3'-primer for amplification of upstream region of URA3 structural gene

<400> 30

gggaagcttc cccagttgta caccaatctt gtcgacag 38

<210> 31

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad1-5 used for destruction of Ogataea minuta ADE1 gene

<400> 31

aaaaagcggc cgctcccggg gtccgcgaga aatctttatg cgtagtcttg 50

<210> 32

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad1-3 used for destruction of Ogataea minuta ADE1 gene

<400> 32

cccccgatc ctttttttta agcttggtgt actccttcca tgcacttccg gtgatg 56

<210> 33

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad2-5 used for destruction of Ogataea minuta ADE1 gene

<400> 33

ttttcacccc gtcaaggatc cctgaacaag gcgaacacga cgaaaacatt tcccccgag 59

<210> 34

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Dad2-3 used for destruction of Ogataea minuta ADE1 gene

<400> 34

tttttgggcc cacctgggtg aagatttgcc agatcaagtt ctcc

44

<210> 35

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DA5 used for confirmation of destruction of Ogataea minuta ADE1 gene

<400> 35

gatgcttgcg ccttcaacca catactcctc

30

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DA3 used for confirmation of destruction of Ogataea minuta ADE1 gene

<400> 36

aaaagttctt gcacagcctc aatattgacc

30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DOU5 used for confirmation
of destruction of Ogataea minuta ADE1 gene

<400> 37

atcgatttcg agtgtttgtc caggtccggg

30

<210> 38

<211> 10

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> variation

<222> 3

<223> Xaa=His or Arg

<220>

<221> variation

<222> 4

<223> Xaa=Ile or Val

<400> 38

Pro Gln Xaa Xaa Trp Gln Thr Trp Lys Val

1 5 10

<210> 39

<211> 11

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 39

Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp

1 5 10

<210> 40

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer POH5 for amplification of 5'-region of Ogataea minuta OCH1 gene

<400> 40

ccncarcryr thtggcarac ntggaargt

29

<210> 41

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer POH3 for amplification of 3'-region of Ogataea minuta OCH1 gene

<400> 41

ccaytgrcar aaytgdanc knckngcrt a cca

33

<210> 42

<211> 2527

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 508..1812

<400> 42

agatctgttg aacttggtca agcgtgtagc caagagaata ggaaacggaa ttccatactg 60
ccggcacaca aggacaataa gggcgtccgg ggctgtcgaa attgtcgaga ccgtagagct 120
attgttacct caataagttg ctctacgatt gtttccgtct ttgacaaagc agtaggcctt 180
tctcaaggtg gtgtacgggt gtttcatttt taatttgcac cgagaacgcg tagtgcgcca 240
atggatctgc agggggctcg gctgattgca ctgaaatttc agcaataaat agctgaggat 300
attcaggcac aacggtacca acggggcagg cttagatcgc aagcagcagg agaaggcagc 360
gaagtgactg aagagacgag aaggagacga atcagcctac ccctggaacc ataaacaaag 420
tcgagccgtt tttttaggga cagaaaccgt tctggatatt tattcgacgc agagactcgg 480
tagtcatctc tacgttcagc acacaccatg aactatcacg acttgtagca tgatagcaaa 540
cggcagtcgt tgatgcgaaa ggcgcgaaag ttcgctgaga tgaacaagaa gttggtggtg 600
gtggtcattt taacgatgta cgttgtgtcg cgtctggcgt cggttggaag cacgaaacag 660

gagtcgattc caggactcac catgaaagag tcagagttag aggtgaattt taaaacattt 720
ggaatggatc tgcagaagcg gaacgagcta ccggccgcaa gtgcaacgct gagagaaaaa 780
ctatcgtttt acttccccta tgaccctgaa aaaccagtgc ccaaccaa atggcagacg 840
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ttcgagagtt ttcgaaagag ctgggattcg attttatcgt ggaggagttg gaaggaattg 2460
aagaggagaa gggaggccac caagaggacg gagagtacac gaccatgtca gacactgacg 2520
tactagt 2527

<210> 43

<211> 434

<212> PRT

<213> *Ogataea minuta*

<400> 434

Met Asn Tyr His Asp Leu Tyr Asp Asp Ser Lys Arg Gln Ser Leu Met

1 5 10 15

Arg Lys Ala Arg Lys Phe Ala Glu Met Asn Lys Lys Leu Val Val Val

20 25 30

Val Ile Leu Thr Met Tyr Val Val Ser Arg Leu Ala Ser Val Gly Ser

35 40 45

Thr Lys Gln Glu Ser Ile Pro Gly Leu Thr Met Lys Glu Ser Glu Leu

50 55 60

Glu Val Asn Phe Lys Thr Phe Gly Met Asp Leu Gln Lys Arg Asn Glu

65 70 75 80

Leu Pro Ala Ala Ser Ala Thr Leu Arg Glu Lys Leu Ser Phe Tyr Phe

85 90 95

Pro Tyr Asp Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr Trp

100 105 110
Lys Val Asp Ile Asn Asp Lys Ser Phe Pro Arg His Phe Arg Lys Phe
115 120 125
Gln Glu Thr Trp Pro Gln Leu Asn Ser Gly Tyr Thr Tyr His Leu Ile
130 135 140
Pro Asp Ser Ile Val Asp Glu Phe Met Arg Ser Leu Phe Ala Asn Val
145 150 155 160
Pro Glu Val Ile Ala Ala Tyr Asn Met Leu Pro Lys Asn Ile Leu Lys
165 170 175
Ala Asp Phe Phe Arg Tyr Leu Val Ile Phe Ala Arg Gly Gly Thr Tyr
180 185 190
Ser Asp Ile Asp Thr Ile Cys Leu Lys Pro Val Asn Glu Trp Ala Thr
195 200 205
Phe Asn Glu Gln Thr Val Ile Ser His Tyr Leu Lys Thr Asn Gly Lys
210 215 220
Thr Ser Gln Leu Pro Glu Val Asp Pro Ser Thr Arg Lys Thr Pro Ile
225 230 235 240
Gly Leu Thr Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His
245 250 255

Glu Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp Thr Ile Gln Gly

260

265

270

Lys Gln Gly His Pro Met Leu Arg Glu Leu Ile Ile Arg Ile Val Glu

275

280

285

Gln Thr Phe Arg Lys Glu Ala Met Gly Asn Leu Lys Lys Val Glu Gly

290

295

300

Lys Asp Met Gly Gly Asp Ile Met Gln Trp Thr Gly Pro Gly Val Phe

305

310

315

320

Thr Asp Thr Leu Phe Asp Tyr Leu Asn Asn Val Val Ser Asp Gly Lys

325

330

335

Leu Gly Asp Gly Tyr Gly Val Gly Ser Lys Tyr Trp Asn Ser His Ala

340

345

350

Lys Tyr Lys Leu Ser His Ile Glu Val Asp Ala Asn Asn Glu Pro Met

355

360

365

His Ser Asp Lys Gln Thr Ile Ser Trp Lys Ser Met Ser Lys Leu Ser

370

375

380

Glu Pro Leu Ile Ile Asp Asp Val Met Ile Leu Pro Ile Thr Ser Phe

385

390

395

400

Ser Pro Gly Val Gly Gln Met Gly Ser His Ser Pro Asp His Pro Leu

405

410

415

Ala Phe Val Arg His Met Phe Gln Gly Ser Trp Lys Pro Asp Ala Glu

420

425

430

Lys Met

<210> 44

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer D03 used for confirmation
of destruction of Ogataea minuta OCH1 gene

<400> 44

ccattgtcag ctccaattct ttgataaacg

30

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer D05 used for confirmation
of destruction of Ogataea minuta OCH1 gene

<400> 45

acacttccgt aagttccaag agacatggcc

30

<210> 46

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer D03-2 used for confirmation
of destruction of Ogataea minuta OCH1 gene.

<400> 46

tcaccacgtt attgagataa tcaaacaggg

30

<210> 47

<211> 8

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 47

Thr Asn Tyr Leu Asn Ala Gln Tyr

1

5

<210> 48

<211> 8

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 48

Lys Ala Tyr Trp Glu Val Lys Phe

1

5

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPA5 for amplification of
5'-region of Ogataea minuta PEP4 gene

<400> 49

acnaaytayy tnaaygcna rta

23

<210> 50

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPA3 for amplification of
3'-region of Ogataea minuta PEP4 gene

<400> 50

aaytnacyt cccartangc ytt

23

<210> 51

<211> 1951

<212> DNA

<213> *Ogataea minuta*

<220>

<221> CDS

<222> 477..1709

<400> 51

catatgtatt catcaatcta cagcttttct aatcngtgtg acttcagtca catgatcctc 60
tgacccgccg cgaccttgct ggcttcacgc gcgcgaaact cactcccaat tttcggatta 120
gctaatacag aagatTTTTG gatttctga tctgtagtgt atccatcctg ccttaatcgt 180
tttcgataca ttgtttatcc gaattgggaa tggcattagt cgtgcgccac ccgactcgcc 240
acccccattc tagtggcaaa caggattgaa agagggctaa aaggtaactt agtgttttat 300
ctctgaatct tccttctgat atcaatcaac aattgttaaa cgattgaaag ttttgaaaca 360
ttcattgaac ttgcgaagcg ctacacacgc atcgttcggt tagcagttac aacagtttag 420
gtttttttcc ccacaaaaag gctcacgctg cctcctcact cttgcctctt ttcttgatga 480
aactctcgct tgcatgtgct gcccttggtg gtttccaaga ggcccacgcc aaggttcatc 540
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 tggatatgtt attgctttta ttacgtgacc aaatgttggt ttttctttca ccttttactc 1860
 tgcactactt cactctttca ttggctttgg aagtacgtta tttttttcac cctatgtaac 1920
 tgaattgcac aaatttaaag attgctctag a 1951

<210> 52

<211> 410

<212> PRT

<213> *Ogataea minuta*

<400> 52

Met Lys Leu Ser Leu Ala Leu Leu Ala Leu Gly Gly Phe Gln Glu Ala

1

5

10

15

His Ala Lys Val His His Ala Pro Ile Lys Lys Thr Pro Ala Ala Glu

20

25

30

Thr Tyr Lys Asp Val Ser Phe Gly Asp Tyr Val Asp Ser Leu Lys Gly

35

40

45

Lys Tyr Val Ser Met Phe Ala Lys His Ala Ala Glu Ser Ser Gln Asn

50

55

60

Ala Phe Val Pro Phe Val Gln Glu Val Gln Asp Pro Glu Phe Thr Val

65

70

75

80

Gln Glu Gly His Asn Ser Pro Leu Thr Asn Tyr Val Asn Ala Gln Tyr

85

90

95

Phe Thr Glu Ile Gln Ile Gly Thr Pro Gly Gln Pro Phe Lys Val Ile

100

105

110

Leu Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Gly Ser Asp Cys Ser

115

120

125

Ser Leu Ala Cys Tyr Leu His Gln Lys Tyr Asp His Asp Ser Ser Ser

130

135

140

Thr Tyr Lys Ala Asn Gly Ser Glu Phe Ala Ile Arg Tyr Gly Ser Gly

145

150

155

160

Ser Leu Glu Gly Phe Val Ser Gln Asp Thr Leu Thr Leu Gly Asp Leu

165

170

175

Ile Ile Pro Lys Gln Asp Phe Ala Glu Ala Thr Ser Glu Pro Gly Leu

180

185

190

Ala Phe Ala Phe Gly Lys Phe Asp Gly Ile Leu Gly Leu Ala Tyr Asp

195

200

205

Thr Ile Ser Val Asp Lys Ile Val Pro Pro Ile Tyr Asn Ala Leu Asn
210 215 220

Leu Gly Leu Leu Asp Glu Pro Gln Phe Ala Phe Tyr Leu Gly Asp Thr
225 230 235 240

Ala Lys Ser Glu Ala Asp Gly Gly Val Ala Thr Phe Gly Gly Val Asp
245 250 255

Glu Thr Lys Tyr Asp Gly Lys Ile Thr Trp Leu Pro Val Arg Arg Lys
260 265 270

Ala Tyr Trp Glu Val Lys Phe Asp Gly Ile Ala Leu Gly Asp Glu Tyr
275 280 285

Ala Thr Leu Asp Gly Tyr Gly Ala Ala Ile Asp Thr Gly Thr Ser Leu
290 295 300

Ile Ala Leu Pro Ser Gln Leu Ala Glu Ile Leu Asn Ser Gln Ile Gly
305 310 315 320

Ala Glu Lys Ser Trp Ser Gly Gln Tyr Thr Ile Asp Cys Glu Lys Arg
325 330 335

Ala Ser Leu Pro Asp Leu Thr Phe Asn Phe Asp Gly Tyr Asn Phe Ser
340 345 350

Ile Ser Ala Tyr Asp Tyr Thr Leu Glu Val Ser Gly Ser Cys Ile Ser
355 360 365

Ala Phe Thr Pro Met Asp Phe Pro Ala Pro Ile Gly Pro Leu Ala Ile

370

375

380

Ile Gly Asp Ala Phe Leu Arg Lys Tyr Tyr Ser Val Tyr Asp Leu Gly

385

390

395

400

Lys Asp Ala Val Gly Leu Ala Lys Ala Val

405

410

<210> 53

<211> 11

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> variation

<222> 2

<223> Xaa=Gly or Leu

<400> 53

Asp Xaa Asn Gly His Gly Thr His Cys Ala Gly

1

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<210> 54

<211> 11

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> variation

<222> 6

<223> Xaa=Ser or Thr

<220>

<221> variation

<222> 9

<223> Xaa=Val or Ile

<220>

<221> variation

<222> 10

<223> Xaa=Ala or Val

<400> 54

Gly Thr Ser Met Ala Xaa Pro His Xaa Xaa Gly

1

5

10

<210> 55

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPB5 for amplification of
5'-region of Ogataea minuta PRB1 gene

<400> 55

gaybknaayg gncayggnac ncaytgykcn gg

32

<210> 56

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PPB3 for amplification of
3'-region of Ogataea minuta PRB1 gene

<400> 56

ccnrcnayrt gnggnwsngc catnwsngtn cc

32

<210> 57

<211> 2214

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 394..2013

<400> 57

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cagatcccaa atttgccacc agactaaatt ggggcattct ggtgagggaa taggggaaat 180
aagagggtgt tttgacgttt catatacatt gctctttctt ttcttggacg gttagcggta 240
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tttcaagttg cttccaatat tgtttgtcca gattagagtc attgcttgaa gctt 2214

<210> 58

<211> 539

<212> PRT

<213> *Ogataea minuta*

<400> 58

Met Lys Leu Ser Gln Ser Ala Ala Val Ala Ile Leu Ser Ser Leu Ala

1 5 10 15

Ala Val Glu Ala Leu Val Ile Pro Leu Phe Asp Asp Leu Pro Ala Glu

20 25 30

Phe Ala Leu Val Pro Met Asp Ala Lys Ala Glu Val Ile Ser Asp Val

35 40 45

Pro Val Asp Ser Ala Ile Ser Asp Ala Pro Ile Ala Ala Leu Asn Asp

50 55 60

Ala Pro Ser Pro Leu Val Thr Ser Leu Ile Ala Ser Gln Asn Leu Ile

65 70 75 80

Pro Asn Ser Tyr Ile Val Val Phe Lys Asn Gly Leu Ala Ser Gly Ala

85 90 95

Val Asp Phe His Met Glu Trp Leu Lys Glu Thr His Ser Gln Thr Leu

100 105 110
Ala Ala Leu Ser Lys Asp Met Pro Ala Glu Glu Leu Ala Ala Glu Gly
115 120 125
Phe Val Ser Glu Ser Ile Asp Leu Thr Glu Val Phe Ser Ile Ser Asp
130 135 140
Leu Phe Ser Gly Tyr Thr Gly Tyr Phe Pro Glu Lys Val Val Asp Leu
145 150 155 160
Ile Arg Arg His Pro Asp Val Ala Phe Val Glu Gln Asp Ser Arg Val
165 170 175
Phe Ala Asp Lys Ser Ser Thr Gln Asn Gly Ala Pro Trp Gly Leu Ser
180 185 190
Arg Ile Ser His Arg Glu Pro Leu Ser Leu Gly Asn Phe Asn Glu Tyr
195 200 205
Val Tyr Asp Asp Leu Ala Gly Asp Gly Val Thr Ala Tyr Val Ile Asp
210 215 220
Thr Gly Ile Asn Val Lys His Glu Gln Phe Gly Gly Arg Ala Glu Trp
225 230 235 240
Gly Lys Thr Ile Pro Thr Gly Asp Asp Asp Ile Asp Gly Asn Gly His
245 250 255

Gly Thr His Cys Ala Gly Thr Ile Gly Ser Glu Asp Tyr Gly Val Ser
260 265 270

Lys Asn Ser Lys Ile Val Ala Val Lys Val Leu Arg Ser Asn Gly Ser
275 280 285

Gly Ser Met Ser Asp Val Ile Lys Gly Val Glu Phe Ala Ala Asn Asp
290 295 300

) His Val Ala Lys Ser Lys Ala Lys Lys Asp Gly Phe Lys Gly Ser Thr
305 310 315 320

Ala Asn Met Ser Leu Gly Gly Gly Lys Ser Pro Ala Leu Asp Leu Ala
325 330 335

Val Asn Ala Ala Val Lys Ala Gly Leu His Phe Ala Val Ala Ala Gly
340 345 350

) Asn Asp Asn Ala Asp Ala Cys Asn Tyr Ser Pro Ala Ala Ala Glu Asn
355 360 365

Ala Val Thr Val Gly Ala Ser Thr Leu Ser Asp Ser Arg Ala Tyr Phe
370 375 380

Ser Asn Tyr Gly Lys Cys Val Asp Ile Phe Ala Pro Gly Leu Asn Ile
385 390 395 400

Leu Ser Thr Tyr Ile Gly Ser Asp Thr Ala Thr Ala Thr Leu Ser Gly
405 410 415

Thr Ser Met Ala Ser Pro His Val Cys Gly Leu Leu Thr Tyr Phe Leu

420

425

430

Ser Leu Gln Pro Glu Ser Ser Ser Leu Phe Ser Ser Ala Ala Ile Ser

435

440

445

Pro Ala Gln Leu Lys Lys Asn Leu Ile Lys Phe Gly Thr Lys Asn Val

450

455

460

Leu Ser Glu Ile Pro Ser Asp Gly Thr Pro Asn Ile Leu Ile Tyr Asn

465

470

475

480

Gly Ala Gly Lys Asn Ile Ser Asp Phe Trp Ala Phe Glu Asp Glu Ala

485

490

495

Ser Ala Lys Ser Asp Leu Lys Lys Ala Val Asp Ile Ala Thr Ser Val

500

505

510

Asp Leu Asp Leu Gln Asp Ile Lys Glu Lys Phe Asn His Ile Leu Glu

515

520

525

Glu Val Ala Glu Glu Val Ala Asp Leu Phe Asp

530

535

<210> 59

<211> 9

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> variation

<222> 1

<223> Xaa=His or Asn

<220>

<221> variation

<222> 5

<223> Xaa=Val or Thr

<400> 59

Xaa Tyr Asp Trp Xaa Phe Leu Asn Asp

1

5

<210> 60

<211> 12

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 60

Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile

1

5

10

<210> 61

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PKR5 for amplification of
5'-region of Ogataea minuta KTR1 gene

<400> 61

maytaygayt ggrynttyyt naayga

26

<210> 62

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PKR3 for amplification of
3'-region of Ogataea minuta KTR1 gene

<400> 62

atytcraft tnsccarar rtgrcanarr ttrta

35

<210> 63

<211> 1930

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 124..1335

<400> 63

gagctctata tttagctttg gacattggta ctagttggac tgttgatcgg ttgacttgac 60
agtgagttct atagaaagac aggctacaaa gaccaccaag gctggcaaatt ttgcgagatt 120
acaatggcta gagcgaatgc gaggtgatc cggtttgcaa tctttgctac cgtgttggtt 180
ttatgtggat acattttatc caagggctcg tctacttcgt atacgatttc gacgccagag 240
tccggctcga gttccagtgg cactgttgct aatactgaga aatctgccct cgcagtgggt 300
gagaaaagcg ttgcaggcgc agccgagaaa agcgttcctg cagctgacgt cccagatgga 360
aaggtgaagg ccacttttgt ctctttggcc agaaaccagg atctgtggga gctgggtgaac 420
tcgatcagac aggtcgaaga ccgtttcaac aacaagtatc attacgattg ggtgttcttg 480
aacgacgcgg aattcaacga cgagttcaag aaggtgacct ctcaggtctg ttcgggtaag 540
accaagtatg gtgtcattcc aaaggaacag tggagcttcc cttcgtggat cgacactgat 600
aaggctgctg ccaccagaga gcaaatgaga aaggacaaga tcatctacgg agactccatc 660
tcgtacagac acatgtgcag atacgagtcg ggattcttct tcaaacaccc agaactcgca 720
gagtacgagt actactggag agtggagcca agcatcaaga tctactgtga cattgactac 780
gacatcttca agttcatgaa ggacaacaag aagtcgtacg gatggaccat ttctcttcc 840
gagtacaagg agaccatccc aactctgtgg aagaccacta gagacttcat gaaggaaaac 900
ccacagtacg ttgcccagga caacctgatc aactttatit cggacgacgg aggaagcagc 960
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ccaattgggtt tacgaggttag gatgggactt accaccgatac atattcagct tcctggactc 1860
tgaatcttcg cccagtgagg ggctgatgaa cagcaaggtc acggttcttt tcttgaagct 1920
gtttgagctc 1930

<210> 64

<211> 403

<212> PRT

<213> *Ogataea minuta*

<400> 64

Met Ala Arg Ala Asn Ala Arg Leu Ile Arg Phe Ala Ile Phe Ala Thr

1

5

10

15

Val Leu Val Leu Cys Gly Tyr Ile Leu Ser Lys Gly Ser Ser Thr Ser

20

25

30

Tyr Thr Ile Ser Thr Pro Glu Ser Gly Ser Ser Ser Ser Gly Thr Val

35

40

45

Ala Asn Thr Glu Lys Ser Ala Leu Ala Val Gly Glu Lys Ser Val Ala

50

55

60

Gly Ala Ala Glu Lys Ser Val Pro Ala Ala Asp Val Pro Asp Gly Lys

65

70

75

80

Val Lys Ala Thr Phe Val Ser Leu Ala Arg Asn Gln Asp Leu Trp Glu

85

90

95

Leu Val Asn Ser Ile Arg Gln Val Glu Asp Arg Phe Asn Asn Lys Tyr
100 105 110

His Tyr Asp Trp Val Phe Leu Asn Asp Ala Glu Phe Asn Asp Glu Phe
115 120 125

Lys Lys Val Thr Ser Gln Val Cys Ser Gly Lys Thr Lys Tyr Gly Val
130 135 140

Ile Pro Lys Glu Gln Trp Ser Phe Pro Ser Trp Ile Asp Thr Asp Lys
145 150 155 160

Ala Ala Ala Thr Arg Glu Gln Met Arg Lys Asp Lys Ile Ile Tyr Gly
165 170 175

Asp Ser Ile Ser Tyr Arg His Met Cys Arg Tyr Glu Ser Gly Phe Phe
180 185 190

Phe Lys His Pro Glu Leu Ala Glu Tyr Glu Tyr Tyr Trp Arg Val Glu
195 200 205

Pro Ser Ile Lys Ile Tyr Cys Asp Ile Asp Tyr Asp Ile Phe Lys Phe
210 215 220

Met Lys Asp Asn Lys Lys Ser Tyr Gly Trp Thr Ile Ser Leu Pro Glu
225 230 235 240

Tyr Lys Glu Thr Ile Pro Thr Leu Trp Lys Thr Thr Arg Asp Phe Met
245 250 255

Lys Glu Asn Pro Gln Tyr Val Ala Gln Asp Asn Leu Ile Asn Phe Ile

260

265

270

Ser Asp Asp Gly Gly Ser Ser Tyr Asn Gly Cys His Phe Trp Ser Asn

275

280

285

Phe Glu Val Gly Ser Leu Glu Phe Trp Arg Gly Glu Ala Tyr Thr Lys

290

295

300

Tyr Phe Glu Ala Leu Asp Gln Ala Gly Gly Phe Phe Tyr Glu Arg Trp

305

310

315

320

Gly Asp Ala Pro Ile His Ser Ile Ala Val Ala Leu Phe Met Pro Lys

325

330

335

Asp Glu Val His Phe Phe Asp Asp Val Gly Tyr Phe His Asn Pro Phe

340

345

350

His Asn Cys Pro Ile Asp Asn Ala Val Arg Glu Ala Lys Asn Cys Val

355

360

365

Cys Asn Gln Ala Asp Asp Phe Thr Phe Gln His Tyr Ser Cys Thr Pro

370

375

380

Lys Phe Tyr Gln Glu Met Gly Leu Lys Lys Pro Ala Asn Trp Glu Gln

385

390

395

400

Tyr Ile His

<210> 65

<211> 10

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 65

Thr Ser Trp Val Leu Trp Leu Asp Ala Asp

) 1 5 10

<210> 66

<211> 10

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 66

Glu Thr Glu Gly Phe Ala Lys Met Ala Lys

) 1 5 10

<210> 67

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PMN5 for amplification of
5'-region of Ogataea minuta MNN9 gene

<400> 67

acnwsntggg tnytntggyt ngaygcnga

29

<210> 68

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PMN3 for amplification of
3'-region of Ogataea minuta MNN9 gene

<400> 68

ttngccatyt tngcraance ytcngtytc

29

<210> 69

<211> 2221

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 931..2034

<400> 69

gggcccagag gaggaggtag gagtgggggg atcgccaatt ttctggcgcg ctactcgcgc 60
ctgccccgca cttcggccgc accgccaacc ttttctttgc gcacccccctc tccaacgttt 120
ccggcctttc cattgaagcg agctaagcag tcagagagca ccaccgggag acgtgatcgc 180
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atctttcaga tggccgcagg ttgctggcag cttcgggctg acaacatcat ggctgacgta 300
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gcatcgcagg agtgtaagc ggcagaaaag aggaggtgga gtggggacga gagatccggg 420
taaccgtagt cggcgcgcga gtccgagaag ttaatcgacg cgtcgaaact gggctctttt 480
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 t. 2221

<210> 70

<211> 367

<212> PRT

<213> *Ogataea minuta*

<400> 70

Met Leu Lys Gly Val Leu Lys His Pro Leu Val His Gln Ile Arg Arg

1

5

10

15

Lys Pro Val Lys Val Leu Val Pro Val Phe Gly Leu Ala Val Leu Leu

20

25

30

Phe Leu Val Phe Gly Gly Ser Ser Ser Asn Arg Lys Thr Asn Ser Pro

35

40

45

Tyr Ser Tyr Lys Arg Asn Asn Arg Asp Glu Val Ile Pro Arg Asn Leu

50

55

60

Pro Ala Asp His Ile Ser His Tyr Asp Leu Asn Asn Leu Ala Ser Thr

65

70

75

80

Pro Met Ala Ala Tyr Asn Lys Glu Arg Val Leu Ile Leu Thr Pro Met

85

90

95

Ala Lys Phe Leu Asp Gly Tyr Trp Asp Asn Leu Leu Lys Leu Thr Tyr

100

105

110

Pro Arg Asp Leu Ile Glu Leu Gly Phe Ile Val Pro Arg Thr Ala Glu

115

120

125

Gly Asp Gln Ala Leu Lys Lys Leu Glu His Ala Val Lys Ile Ile Gln

130

135

140

Asn Pro Lys Asn Thr Lys Glu Pro Lys Phe Ala Lys Val Thr Ile Leu

145

150

155

160

Arg Gln Asp Asn Glu Ser Leu Ser Ser Gln Ser Glu Lys Asp Arg His

165

170

175

Ala Phe Lys Val Gln Lys Glu Arg Arg Ala Gln Met Ala Thr Ala Arg

180

185

190

Asn Ser Leu Leu Phe Thr Thr Ile Gly Pro Tyr Thr Ser Trp Val Leu

195

200

205

Trp Leu Asp Ser Asp Ile Val Glu Ser Pro His Thr Leu Ile Gln Asp

210

215

220

Leu Val Ser His Asp Lys Pro Val Ile Ala Ala Asn Cys Tyr Gln Arg

225

230

235

240

Tyr Tyr Asp Glu Asp Lys Lys Glu Asp Ser Ile Arg Pro Tyr Asp Phe

245 250 255
Asn Asn Trp Ile Glu Ser Glu Glu Gly Leu Arg Ile Ala Ser Thr Met
260 265 270
Ser Asp Asp Glu Ile Ile Val Glu Ala Tyr Ala Glu Ile Ala Thr Tyr
275 280 285
Arg Pro Leu Met Gly His Phe Tyr Asp Pro Asn Gly Asp Leu Gly Thr
290 295 300
Glu Met Gln Leu Asp Gly Val Gly Gly Thr Cys Leu Met Val Lys Ala
305 310 315 320
Asp Val His Arg Asp Gly Ala Met Phe Pro Asn Phe Pro Phe Tyr His
325 330 335
Leu Ile Glu Thr Glu Gly Phe Ala Lys Met Ala Lys Arg Leu Gly Tyr
340 345 350
Gln Val Phe Gly Leu Pro Asn Tyr Leu Val Phe His Tyr Asn Glu
355 360 365

<210> 71

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DMN5

<400> 71

agatgagggtg attccacgta atttgccagc

30

<210> 72

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DMN3

<400> 72

ttttgattgt catctatttc gcacaccctg

30

<210> 73

<211> 12

<212> PRT

<213> Pichia pastoris

<400> 73

Gly Gly Gly Ser Ser Ile Asn Phe Met Met Tyr Thr

1

5

10

<210> 74

<211> 10

<212> PRT

<213> Pichia pastoris

<400> 74

Asp Met Trp Pro Met Val Trp Ala Tyr Lys

1 5 10

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAX5 for amplification of
5'-region of Ogataea minuta AOX1 gene

<400> 75

ggngnggnw snwsnathaa yttyatgatg tayac 35

<210> 76

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PAX3 for amplification of
3'-region of Ogataea minuta AOX1 gene

<400> 76

tttrtangccc anaccatngg ccacatrtc 29

<210> 77

<211> 5817

<212> DNA

<213> *Ogataea minuta*

<220>

<221> CDS

<222> 2349..4340

<400> 77

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<211> 663

<212> PRT

<213> *Ogataea minuta*

<400> 78

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1

5

10

15

Cys Gly Cys Ala Ile Ala Gly Arg Leu Gly Asn Leu Asp Pro Asp Val

20

25

30

Thr Val Ala Leu Ile Glu Gly Gly Glu Asn Asn Ile Asn Asn Pro Trp

35

40

45

Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys

50

55

60

Thr Ala Thr Phe Tyr Asn Ser Arg Pro Ser Lys His Leu Asn Gly Arg

65

70

75

80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile

85

90

95

Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp Trp

100

105

110

Glu Gln Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Lys

115

120

125

Leu Glu Thr Tyr Gln Arg Pro Cys Asn Asn Arg Glu Val His Gly Phe

130

135

140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Thr Ala

145

150

155

160

Gln Asp Phe Leu Arg Ala Cys Glu Ser Gln Gly Ile Pro Phe Asn Asp

165 170 175
Asp Leu Glu Asp Leu Lys Ala Ser His Gly Ala Glu Tyr Trp Leu Lys
180 185 190
Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala Tyr
195 200 205
Ile His Pro Thr Met Arg Asn Lys Ser Asn Leu Phe Leu Ile Thr Ser
210 215 220
Thr Lys Ala Asp Lys Val Ile Ile Glu Asn Gly Val Ala Val Gly Val
225 230 235 240
Arg Thr Val Pro Met Lys Pro Val Glu Thr Lys Asn Pro Pro Ser Arg
245 250 255
Ile Phe Lys Ala Arg Lys Gln Ile Val Val Ser Cys Gly Thr Ile Ser
260 265 270
Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ala Ala His Lys Leu
275 280 285
Arg Gln Ala Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly Glu
290 295 300
Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr Tyr Ser Lys Pro
305 310 315 320

Glu Val Pro Thr Phe Asp Asp Phe Val Arg Gly Asp Pro Val Ala Gln
325 330 335

Lys Ser Ala Phe Asp Gln Trp Tyr Ser Asn Lys Asp Gly Pro Leu Thr
340 345 350

Thr Asn Gly Ile Glu Ala Gly Val Lys Ile Arg Pro Thr Asp Glu Glu
355 360 365

Leu Ala Thr Ala Asp Asp Asp Phe Ile Gln Gly Tyr His Glu Tyr Phe
370 375 380

Asp Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Val Ile Ser Gly
385 390 395 400

Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Phe Phe Thr Met
405 410 415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val Tyr Ala Val
420 425 430

Ser Pro Asp Pro Tyr Glu Ala Pro Asp Phe Asp Pro Gly Phe Leu Asn
435 440 445

Asp Ser Arg Asp Met Trp Pro Met Val Trp Ser Tyr Lys Lys Ser Arg
450 455 460

Gln Thr Ala Arg Arg Met Glu Ser Phe Ala Gly Glu Val Thr Ser His
465 470 475 480

His Pro Leu Tyr Pro Val Asp Ser Pro Ala Arg Ala Lys Asp Leu Asp

485

490

495

Leu Glu Thr Cys Lys Ala Phe Ala Gly Pro Asn His Phe Thr Ala Asn

500

505

510

Leu Tyr His Gly Ser Trp Thr Val Pro Ile Glu Lys Pro Thr Pro Lys

515

520

525

Asn Asp Ser His Val Thr Cys Asn Gln Val Glu Ile Phe Ser Asp Ile

530

535

540

Asp Tyr Ser Ala Glu Asp Asp Glu Ala Ile Val Lys Tyr Ile Lys Glu

545

550

555

560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala Pro

565

570

575

Gln Glu Gly Ser Lys Ile Ala Pro Lys Gly Gly Val Val Asp Ala Arg

580

585

590

Leu Asn Val Tyr Glu Val Lys Asn Leu Lys Val Ala Asp Leu Ser Ile

595

600

605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Ser Thr Ala Leu Leu Ile

610

615

620

Gly Glu Lys Ala Ala Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser Gly

625

630

635

640

Ser Asp Leu Ala Met Thr Ile Pro Asn Phe Lys Leu Gly Thr Tyr Glu

645

650

655

Glu Lys Gly Leu Ala Arg Phe

660

<210> 79

<211> 2348

<212> DNA

<213> *Ogataea minuta*

<400> 79

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cgaaaaaa 2348

<210> 80

<211> 802

<212> DNA

<213> *Ogataea minuta*

<400> 80

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 actgcccgtg ccactaacgg ta 802

<210> 81

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAP5 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 81

ctgcagcccc ttctgttttt cttttgacgg

30

<210> 82

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAP3 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 82

cccccgatc caggaaccg ggaacagaat ctagattttt tcgtaagtcg taagtcgtaa 60
cagaacacaa gagtctttga acaagttgag 90

<210> 83

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAT5 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 83

cccccccgga tccgagacgg tgcccgactc ttgttcaatt cttttgg 47

<210> 84

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer OAT3 for production of an expression cassette with AOX1 gene promoter and terminator

<400> 84

cccataatgg taccgttagt ggtacgggca gtc

33

<210> 85

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer HGP5 for amplification of a gene conferring resistance against hygromycin B

<400> 85

gtcgacatga aaaagcctga actcaccgc

29

<210> 86

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer HGP3 for amplification of a gene conferring resistance against hygromycin B

<400> 86

actagtctat tcctttgccc tcggacg

27

<210> 87

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of 5'-region of α -mannosidase gene

<400> 87

ggggggtcga catggtggtc ttcagcaaaa ccgctgccc

39

<210> 88

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of 5'-region of α -mannosidase gene

<400> 88

ggggggcggc cgcgatgatgt tgagggtgtt gtacggaacc ccc

43

<210> 89

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of
Saccharomyces cerevisiae SUC2 gene

<400> 89

ggggactagt atgcttttgc aagctttcct tttccttttg

40

<210> 90

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for amplification of
Saccharomyces cerevisiae SUC2 gene

<400> 90

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39

<210> 91

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..711

<400> 91

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<210> 92

<211> 234

<212> PRT

<213> Homo sapiens

<400> 92

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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser

20

25

30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val
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Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
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Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
100 105 110

Ser Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 93

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..1428

<400> 93

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<210> 94

<211> 475

<212> PRT

<213> Homo sapiens

<400> 94

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Val Gln Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys

20

25

30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45
Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
65 70 75 80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Asp Arg Ile Ile Met Val Arg Gly Val Tyr Tyr
115 120 125
Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
130 135 140
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145 150 155 160
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225 230 235 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
260 265 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
275 280 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
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Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

355

360

365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp

370

375

380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

385

390

395

400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

405

410

415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

420

425

430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

435

440

445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

450

455

460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

465

470

475

<210> 95

<211> 7

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 95

Val Gly Phe Leu Asp His Met

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<210> 96

<211> 7

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 96

Pro Ser Thr Lys Gly Val Leu

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<210> 97

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer PHI5 for amplification of
Ogataea minuta HIS3 gene

<400> 97

tnggnttyyt ngaycayatg

20

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PHI3 for amplification of
Ogataea minuta HIS3 gene

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arnacnccyt tngtnswngg

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<210> 99

<211> 3831

<212> DNA

<213> Ogataea minuta

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<221> CDS

<222> 1839..2552

<400> 99

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<211> 238

<212> PRT

<213> Ogataea minuta

<400> 100.

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20 25 30

Ser Ile Gln Ile Ile Leu Asn Leu Asp Gly Gly Leu Ile Glu Cys Lys

35 40 45

Glu Ser Ile Leu Gly Ala Thr Tyr Glu Lys Glu Ser His Ala Ala Gln

50 55 60

Asn Thr Ser Ala Gln Val Ile Ser Ile Lys Thr Gly Leu Gly Phe Leu

65 70 75 80

Asp His Met Leu His Ala Leu Ala Lys His Ser Gly Trp Ser Leu Ile

85 90 95

Val Glu Cys Ile Gly Asp Leu His Ile Asp Asp His His Thr Ala Glu

100 105 110

Asp Val Gly Ile Ala Leu Gly Glu Thr Phe Lys Arg Ala Leu Gly Pro

115 120 125

Val Lys Gly Leu Lys Arg Phe Gly His Ala Tyr Ala Pro Leu Asp Glu

130 135 140

Ala Leu Ser Arg Ala Val Val Asp Leu Ser Asn Arg Pro Phe Ala Val
145 150 155 160

Val Glu Leu Gly Leu Arg Arg Glu Lys Ile Gly Asp Leu Ser Cys Glu
165 170 175

Met Ile Pro His Val Leu Glu Ser Phe Ala Thr Ser Ala His Ile Thr
180 185 190

Met His Val Asp Cys Leu Arg Gly Phe Asn Asp His His Arg Ser Glu
195 200 205

Ser Ala Phe Lys Ala Leu Ala Val Ala Ile Arg Asp Ala Thr Ser Tyr
210 215 220

Thr Gly Arg Asp Asp Val Pro Ser Thr Lys Gly Val Leu Met
225 230 235

<210> 101

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DHI5

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<210> 102

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DH13

<400> 102

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<210> 103

<211> 8

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 103

Ala Val Gly Gly Pro Lys Trp Gly

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<210> 104

<211> 7

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 104

Ala Ala Met Met Leu Lys Leu

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<210> 105

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE5 for amplification of
Ogataea minuta LEU2 gene

<400> 105

gcngtnggng gncnaartg ggg

23

<210> 106

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE3 for amplification of
Ogataea minuta LEU2 gene

<400> 106

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21

<210> 107

<211> 5615

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1606..2694

<400> 107

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<210> 108

<211> 363

<212> PRT

<213> *Ogataea minuta*

<400> 108

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Glu Val Val Asp Glu Ala Val Lys Val Leu Asn Ala Ile Ser Ala Ala

20 25 30

Lys Pro Glu Ile Lys Phe Asn Phe Glu His His Leu Ile Gly Gly Ala

35 40 45

Ala Ile Asp Ala Thr Gly Gln Pro Ile Thr Asp Ala Ala Leu Glu Ala
50 55 60

Ser Lys Lys Ala Asp Ala Val Leu Leu Gly Ser Val Gly Gly Pro Lys
65 70 75 80

Trp Gly Thr Gly Gln Val Arg Pro Glu Gln Gly Leu Leu Lys Ile Arg
85 90 95

Lys Glu Leu Asn Leu Tyr Ala Asn Leu Arg Pro Cys Ser Phe Ala Ser
100 105 110

Asp Ala Leu Leu Asp Leu Ser Pro Leu Lys Pro Glu Ile Val Arg Gly
115 120 125

Thr Asp Phe Val Val Val Arg Glu Leu Val Gly Gly Ile Tyr Phe Gly
130 135 140

Glu Arg Lys Glu Asp Asp Gly Ser Gly Phe Ala Ser Asp Thr Glu Ala
145 150 155 160

Tyr Ser Val Pro Glu Val Gln Arg Ile Thr Arg Met Ala Ala Phe Met
165 170 175

Ala Leu Gln Ser Asp Pro Pro Leu Pro Val Tyr Ser Leu Asp Lys Ala
180 185 190

Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu Thr
195 200 205

Ile Lys Asn Glu Phe Pro Gln Leu Lys Leu Gln His His Leu Ile Asp

210

215

220

Ser Ala Ala Met Ile Leu Val Lys Ser Pro Thr Lys Leu Asn Gly Val

225

230

235

240

Val Leu Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala Ser

245

250

255

Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala Ser

260

265

270

Leu Pro Asp Ser Asn Glu Ala Phe Gly Leu Tyr Glu Pro Cys His Gly

275

280

285

Ser Ala Pro Asp Leu Ala Lys Gly Leu Val Asn Pro Leu Ala Thr Ile

290

295

300

Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Leu Val Glu Glu

305

310

315

320

Gly Arg Ala Val Glu Lys Ala Val Arg Ala Val Leu Asp Gln Gly Ile

325

330

335

Met Thr Ala Asp Leu Gly Gly Ser Ser Ser Thr Thr Glu Val Gly Asp

340

345

350

Ala Val Ala Lys Glu Val Thr Lys Leu Leu Gly

355

360

<210> 109

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DL5

<400> 109

caggagctac agagtcacgc

20

<210> 110

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DL3

<400> 110

acgagggaca ggctgctcgc

20

<210> 111

<211> 8

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 111

Asp Thr Gly Ser Ser Asp Leu Trp

1

5

<210> 112

<211> 8

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 112

Phe Gly Ala Ile Asp His Ala Lys

1

5

<210> 113

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE5 for amplification of
Ogataea minuta YPS1 gene

<400> 113

gayacngght cntcngayyt ntgg

24

<210> 114

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PLE3 for amplification of
Ogataea minuta YPS1 gene

<400> 114

ttygghgcna tygaycaygc naa

23

<210> 115

<211> 3661

<212> DNA

<213> Ogataea minuta

<220>

<221> CDS

<222> 1712..3523

<400> 115

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<210> 116

<211> 604

<212> PRT

<213> *Ogataea minuta*

<400> 116

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1

5

10

15

Gly Glu Ser Lys Ala Asn Ser Ser Pro Gly Tyr Leu Arg Met Glu Ala

20

25

30

Glu Ile Tyr Arg Gly His Ser Phe Glu Thr Ser Gln Arg Gly Gly Arg

35

40

45

Pro Tyr Met Leu Glu Lys Arg Ala Glu Asp Gly Ser Val Leu Met Glu

50

55

60

Leu Gln Asn Asn Gln Ser Phe Tyr Lys Val Glu Leu Glu Val Gly Ser

65

70

75

80

Asp Lys Gln Lys Ile Gly Val Leu Val Asp Thr Gly Ser Ser Asp Leu

85

90

95

Trp Ile Met Asn Gln Asn Asn Ser Tyr Cys Glu Ser Ser Ser Ser Ser

100

105

110

Ser Lys Met Arg Glu Arg Lys Gly Arg Lys Leu Ser Asp Leu Arg Asn

115

120

125

Leu Asn Leu Asp Val Ser Glu Lys Asn Val Lys Ala Val Gly Ala Ala

130

135

140

Glu Thr Glu Thr Met Thr Leu Ser Val Gly Glu Gly Leu Phe Ser Trp

145

150

155

160

Phe Glu Thr Gln Thr Asp Gly Ser Gly Gly Glu Thr Glu Thr Ala Ser
165 170 175

Gly Asp Ser Ser Glu Ala Thr Ile Asp Cys Ser Val Tyr Gly Thr Phe
180 185 190

Asp Pro Ser Ser Ser Asp Thr Phe Lys Ser Asn Gly Thr Glu Phe Ser
195 200 205

Ile Ser Tyr Ala Asp Asp Ser Phe Ala Lys Gly Thr Trp Gly Thr Asp
210 215 220

Asp Val Thr Phe Asn Gly Val Thr Val Asp Gln Leu Ser Met Ala Ile
225 230 235 240

Ala Asp Glu Thr Asn Ser Ser Met Gly Val Leu Gly Ile Gly Leu Lys
245 250 255

Gly Leu Glu Thr Thr Tyr Ser Gly Asp Val Thr Asn Ala Tyr Thr Tyr
260 265 270

Glu Asn Leu Pro Tyr Lys Met Gln Ser Gln Gly Leu Ile Ser Lys Pro
275 280 285

Val Tyr Ser Val Tyr Leu Asn Asp Ser Glu Ser Ser Ala Ala Ser Ile
290 295 300

Leu Phe Gly Ala Val Asp His Asp Lys Tyr Thr Gly Thr Leu Thr Leu

305

310

315

320

Leu Pro Ile Ile Asn Thr Ala Glu Ser Leu Gly Tyr Ser Thr Pro Val

325

330

335

Arg Leu Glu Val Thr Leu Ser Lys Leu Tyr Thr Gly Ser Ser Ser Asn

340

345

350

Lys Thr Ala Val Ser Ile Ala Ser Gly Ala Ala Ala Ala Leu Leu Asp

355

360

365

Thr Gly Thr Thr Leu Thr Tyr Val Pro Ser Asp Ile Ile Ser Thr Ile

370

375

380

Val Asp Gln Tyr Gly Phe Gln Tyr Ser Ser Ser Val Gly Thr Tyr Val

385

390

395

400

Ala Lys Cys Asp Ser Leu Asp Asp Ala Glu Ile Val Phe Asp Phe Gln

405

410

415

Gly Thr Lys Ile Trp Val Pro Phe Ser Ser Phe Ala Val Ser Leu Thr

420

425

430

Thr Asn Gly Gly Ser Gln Ser Ser Tyr Cys Ala Leu Gly Leu Met Asp

435

440

445

Ser Gly Asp Asp Thr Phe Thr Leu Gly Asp Ser Phe Leu Asn Asn Val

450

455

460

Tyr Phe Val Ala Asp Leu Glu Asn Leu Gln Ile Ala Ile Ala Pro Ala

465 470 475 480

Asn Leu Asp Ser Thr Ser Glu Asp Ile Glu Val Val Ser Asp Ser Gly

485 490 495

Ile Pro Ser Ala Lys Ser Ala Ser Ala Tyr Ser Ser Ser Trp Gly Ala

500 505 510

Ser Gly Ser Ala Val Ala Ser Ser Leu Ser Val Gln Thr Gly Ala Glu

515 520 525

Thr Val Thr Ser Thr Asp Ala Gly Ser Asp Ser Thr Gly Ser Ala Ser

530 535 540

Gly Ser Ser Gly Ser Ala Ser Ser Ser Ser Ser Lys Ser Ser Ala Ser

545 550 555 560

Ser Ser Ser Gly Ser Ser Gly Ser Ser Ser Lys Ser Gly Ser Ser Ser

565 570 575

Ser Lys Tyr Ala Ala Gly Asn Ala Trp Gly Met Ser Val Cys Ser Leu

580 585 590

Ala Phe Thr Ile Ala Val Ser Val Leu Val Ile Gly

595 600

<210> 117

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DY5

<400> 117

ctcaagggcc tggagactac g

21

<210> 118

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer DY3

<400> 118

cgggattccc gagtcgctca cc

22

<210> 119

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PDI5 for amplification of
5'-region of Saccharomyces cerevisiae PDI gene

<400> 119

tctagaatga agttttctgc tggcgccgctc ctg

33

<210> 120

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer PDI3 for amplification of
3'-region of Saccharomyces cerevisiae PDI gene

<400> 120

ggatccttac aattcatcgt gaatggcatc ttc

33